

Name: Kaplan, B.

Project: PSYCHOPH

Department: Psychiatry

Project Description: The general nature of the project is the investigation of the relation of automatic nervous system (ANS) responses to attentional sets (thinking and environmental observation). In a recently completed study, which examined ANS changes as a function of verbalization and environmental attention and rejection, ACME was used to obtain heart rate and skin conductance values from raw data. This physiological data was then analyzed, using analysis of variance and other parametric statistical procedures. In addition, ACME was used for obtaining correlations between the physiological responses and personality variables.

Future work will look at ANS responses in lactating and non-lactating human females and will investigate ANS correlates of attention and information processing. ACME will be used for transformation of the raw physiological data into meaningful units and the statistical analysis of this data.

Name: Kapp, D.

Project: CHBR

Department: Radiology

Project Description: Data analysis of sedimentation patterns of DNA following X-irradiation.

Name: Kessler, S.

Project: MATSPEED

Department: Psychiatry

Project Description: Will be analyzing mating speed experiments as previously, including use of linear regression and analysis of variance programs.

Name: Kriss, J.

Project: BLDVOL1

Department: Nuclear Medicine

Project Description: The program is being used to calculate plasma volume, blood volume and red cell mass in patients who receive radioactive tracer material. The determination is useful in the evaluation of patients with anemia and polycythemia.

Name: Lederberg, J.

Project: GENLIB1

Department: Genetics

Project Description: This project contains the statistical and miscellaneous programs used by the Genetics Department.

Statistical programs: General statistical analysis for the calculations of sum, mean, standard deviation, the analysis of variance, chisquare and probability of chisquare distribution, correlation and regression analysis, the normal distribution with the same mean and standard deviation for fitting a curve.

Plotting Programs: Plot bar graph in 100 positions, plot of percentage distribution, plot by function scaled to the range of 0 to 100, plot of multivalued function allows the choice and supersition of several characters. Flag is inserted on the chart when underflow or overflow occurred.

Sorting Programs: Sorting a vector in ascending order, sort array and alphabetical informations.

Name: Leiderman, P.

Project: PREMIE

Department: Psychiatry

Project Description: Studies of maternal behavior in non-human mammals have suggested that the degree of interaction permitted between mother and infant in the postpartum period influences later maternal attachment and infant development.

Assessments of each mother and her infant are made periodically during the time the infant is hospitalized and during the first two years at home. Three major areas are included in these assessments: 1) maternal attitudes regarding her relationship with the child as reflected in responses to interviews and questionnaires, 2) maternal behavior observed during routine caretaking of the infant, and 3) the behavioral development of the infant.

Analyses will be done comparing the different groups on various attitudinal and behavioral dimensions at specific points in time as well as changes within groups over the two year period. We will also examine the interrelationships between variables as well as the effects of birth order and sex of the infant on the variables of interest.

Name: Luetscher, J.

Project: Blood-pr

Department: Medicine - Metabolic Research

Project Description: Our research project deals with the secretion and metabolism of adrenal hormones. Various steroid hormones, catecholamines, and trophic hormones are measured under different conditions of sodium loading or sodium depletion. We attempt to define and relate groups of measurements which assist in the identification of curable forms of hypertension.

The ACME system is used in this project in several ways:

(1) To assist in the calculation of laboratory data, involving difficult procedures, such as the double isotope derivative method, which requires solution of simultaneous equations.

(2) Interpretation of data: (a) Simulation of complex systems (for example, the study of reactions in which substrate and enzyme concentrations are regulated by different systems and may vary independently; or distribution and metabolism of hormones). (b) Statistical analysis (comparison of mean and variance of different groups, or correlations between different observations). (c) Analysis of clinical information (the association between different observations, or the effects of drugs, diets, etc.).

(3) Data files are used to store information at various stages of a sequential process, and for collection and analysis of the large amount of clinical and laboratory data which accumulates during a long investigation.

(4) The computer has been used extensively in research training of fellows and staff, first in principles and techniques of computer use, and subsequently in practical applications.

Name: Melges, F.

Project: TEMPO

Department: Psychiatry

Project Description: Relating changes in temporal experience to changes in psychopathological symptoms such as depersonalization and delusions. Our plan is to discover how aberrations in temporal sequencing and distinguishing memories from perceptions and expectations relate to the emergence of definable psychopathological processes. The overall notion for a number of sub-projects is: confusing past, present, and future underlies the central symptoms of psychosis.

Sub-projects involve specific attention to drug-induced psychoses and certain symptoms of psychoses, especially depersonalization, changes in body image, paranoid delusions, and feelings of influence or alien control.

Previous work has demonstrated that this approach is highly useful for understanding psychotic processes. Although aggregate data across subjects will be used, the usual approach will be the intensive study of single subjects as they change over time. This allows for the study of what changes with what over time. In other words, various processes, i.e. sequential relationships between changes, are discovered by this intensive approach.

Name: Miller, R.

Project: BIOSTOP

Department: Community & Preventive Medicine

Project Description: The Division of Biostatistics, Department of Community and Preventive Medicine, provides biostatistical consulting to persons doing medical research in the Stanford Medical Center and occasionally elsewhere, such as Presbyterian Hospital in San Francisco.

Biostatistics also trains postdoctoral fellows and some graduate students in Statistics in biostatistical consulting. Investigations of statistical methods may also be done by the staff, postdoctoral fellows, or graduate students.

The ACME computer is used in all these activities.

Name: Miller, R.

Project: THESES

Department: Community & Preventive Medicine

Project Description: This "project" will be used for computing done by or for graduate students in statistics and biostatistics as part of the research necessary for their theses, or otherwise connected with their education.

Name: Miller, R.

Project: COURSES

Department: Community & Preventive Medicine

Project Description: This "project" will be used for computing done by or for the staff in connection with the teaching of courses in biostatistics.

Name: Nelsen, T.

Project: ADRENAL

Department: Surgery

Project Description: Clinical cancer research record protocols and data for storage and analysis. Next step will be display routines.

Name: Payne, R.

Project: SERNAL

Department: Medicine - Hematology

Project Description: The research is concerned with extending and classification of leukocyte and/or tissue antigens by serologic and genetic analysis of specific human antisera. In the computer programs, 1) donor-recipient pairs of individuals are selected for deliberate immunization to produce antisera, and 2) the antisera are analyzed by comparing their reactions with test cells in 2 x 2 tables for associations between them. The significant associations are calculated, and the frequency of positive reactions are determined.

Name: Porter, R.

Project: ATC_KIN

Department: Biochemistry

Project Description: Project ATC_KIN has been used for data processing in the investigation of the steady-state kinetics of the enzyme, aspartate transcarbamylase. The programs were written for curve-fitting the data from different types of kinetics experiments. For example, program "DataFit" employs a simple linear least squares fit to calculate the initial rate of reaction from the raw data, measured as amount of radioactivity versus time of reaction, and converts the result to standard units of specific enzyme activity, using units of concentration.

Other programs calculate the kinetic parameters using a linear least squares fit for the reciprocal transformation, due to Lineweaver and Burke, of the Michaelis-Menten equation. Another program, "Hyper-Fit", was written to fit the non-linear, hyperbolic function of the original Michaelis-Menten equation. The program employs a reiterative procedure of trial-and-error testing for optimal fit. Trial values for the two parameters of the Michaelis-Menten equation are tested for minimizing the residual, and the procedure is reiterated to give a close approximation of the best values.

This computational procedure was refined and optimized for speed, and the program will compute the best values for the two parameters, to an accuracy exceeding that of the data, in less than ten seconds of computer time in a time-sharing environment. This approach proved to be so successful that it was adapted for curve-fitting other, more complex non-linear kinetic equations with more parameters. For example, the non-linear equation describing substrate inhibition, with three parameters, which does not give a simple linear reciprocal transformation, has been employed directly, using this trial-and-error technique. In addition, the family of hyperbolic curves described by the equation for competitive inhibition, with three parameters, has been employed successfully.

The greatest success of this technique has been the use of equations with four parameters for curve-fitting, such as the equations describing non-competitive inhibition and parabolic competitive inhibition. With correspondingly longer times for calculation, these programs have provided quantitative support for the existence of certain reaction intermediates in the pathway of this enzyme mechanism.

These programs make special use of the on-line communication available with the ACME system, especially through the use of options and operator-controlled branchpoints in the programs.

Name: Reaven, G.

Project: DISPLAY

Department: Medicine - Metabolism

Project Description: 1) Derivation of a three compartment model describing disappearance of plasma insulin. 2) Evaluation of the dog as an experimental model for study of insulin distribution in man. 3) Digital on-line computer display to investigate the structure of metabolic systems. Interested in developing models of glucose, insulin, and triglyceride kinetics as related to diabetes mellitus and atherosclerosis. Clinical data obtained from tracer studies are analyzed by the ACME computer through five stages of development. The project DISPLAY includes the third and fourth stage. The third stage contains the program PEEL that automatically obtains the parameters for a linear sum of constant coefficients of a system of linear differential equations. The results are used for the fourth stage. In this phase, the parameters are used for calculation of a theoretical curve which is displayed on a CRT. It is then compared with data which also appears on the CRT. The results of PEEL and SKINNER enable us to change parameters until we obtain a satisfactory visual fit. In this phase, we used the programs RUNGCV, DATA, TDATA, berman, RUNGPLOT, and RUNGFUN. We are now performing similar analysis with respect to triglyceride metabolism and are extending the insulin work. We expect to use the above procedures the entire year and expect to extend stage four and develop stage five for analysis of non-linear metabolic models.

Name: Reaven, G.

Project: FIT

Department: Medicine - Metabolism

Project Description: (See discussion in Project DISPLAY). The final phase is at the present being developed. The results of simulation in stage 4 is to be statistically evaluated to see if the parameters obtained do not violate the statistical limitations of the data. At the moment, we are doing this in batch mode at the Computation Center. However, the most satisfactory results are obtained if the statistical evaluation is coupled to stage 4. We plan to use nonlinear regression techniques to evaluate these parameters. We have developed two programs for this procedure; they are RUNGPOW and EXPOPOW, which call two programs, POWELL and COVARE, which are stored on public file.

Name: Reaven, G.

Project: PAT_DATA

Department: Medicine - Metabolism

Project Description: (See discussion in Project DISPLAY). This project includes stage 1 and stage 2. Stage 1 and stage 2 are support programs for stages 3, 4, and 5. In stage 1, serum endogenous insulin is biologically assayed by the program INSULIN. The program TCCONRAD determines triglyceride concentration and the program DOUBLE estimates the relative weights of data for future statistical analysis. The second stage consists of statistical support programs for evaluation of the results of stage 1. The programs used in this phase are: TEATEST, RAT, CORL, REGRESS, DICK, TG DOSE, RANK, and YOUTEST.

Our research activities also include procedures to determine weight patterns of patients. The program involved in this aspect is BODYCOMP.

Name: Reitan, J.

Project: INDIRECT

Department: Anesthesia

Project Description: We are processing cardiac internal timings collected by non-invasive, indirect techniques in order to monitor the contractile state of the heart under varying loads and drugs.

Name: Rosenberg, S.

Project: MEDONCOL

Department: Medicine-Oncology

Project Description: Patient and disease analysis - primarily to correlate drug responsiveness in cancer patients for educational and research purposes.

Name: Smith, P.

Project: PREMIES

Department: Pediatrics

Project Description: This data will be used in any study involving premature or sick newborn infants cared for in the Stanford nurseries. Such items as birth weight, gestational age, system disease, etc., will be correlated by pairs.

Name: Spevack, A.

Project: CONDIT

Department: Psychiatry

Project Description: Classical conditioning experiments of amygdalectomized and intact monkeys.

Name: Stark, G.

Project: CHAOS

Department: Biochemistry

Project Description: ACME serves two primary functions. First, it is used to analyze data generated from steady state kinetic experiments on enzymes, primarily aspartate transcarbamylase from Eschenchia coli. Second, it is used to process chromatograms generated by an amino acid analyzer. It is also used for various research and educational tasks by graduate students and medical students, such as analyzing the sedimentation velocity of proteins in the ultracentrifuge. Many of the kinetic experiments referred to above could not be done without the services of ACME, since they involve trial and error fitting of several parameters to complex functions. The routine processing of chromatograms on ACME introduces accuracy and dependability not otherwise available.

Name: Stillman, R.

Project: PSYGAME

Department: Psychiatry

Project Description: Our project involves the use of an interactive system for the interviewing and testing of psychiatric patients.

We are attempting to use the computer and a peripheral CRT display for anticipated psychological testing. This includes terms from standard psychological tests and novel tests which the computer is especially suited for.

Name: Stocker, B.

Project: Stm

Department: Medicine - Micro

Project Description: Main project concerns genetics and physiology of Salmonella typhimurium - in particular somatic lipopolysaccharide, flagella and motility, and plasmids, especially R and colicine factors. I am co-investigator in Dr. Esther Lederberg's project, which concerns mainly recombination-deficient mutants in the same organism. Main ACME usage has been 1) in statistical analysis of data from experiments concerning mouse pathogenicity of lipopolysaccharide mutants (estimations of LD50, rate constant for clearance of bacteria from blood stream, harmonic mean times-to-death, significance tests, etc.) and 2) for storage and analysis of extensive stock-culture data concerning strains with numerous genetic markers.

Name: Strickland, R.

Project: GASTRIC

Department: Medicine - G. I. Division

Project Description: I am involved in clinical research projects relating to gastric secretory function tests and have used the ACME Computer Facility over the past year for filing of data collected from these projects and for statistically analyzing the results obtained.

Name: Summerlin, W.

Project: BIOCHEM

Department: Dermatology

Project Description: To study biochemical control of collagen formation via proline/hydroxyproline (ratios).

Name: Vosti, K.

Project: VOSTI

Department: Medicine - Infectious Diseases

Project Description: Cross-tabulating variables associated with bacterial infections such as underlying disease, age, year, prior and contemporaneous antibiotics, steroids and immuno-suppressives, appropriateness of treatment, and outcome (survival, death).